

TCGACCCACGCGTCCGGGAGGATCGGGAGTCCGGGAGGATGGGCCGCCGCTAGGCTCGCACTCCGGA
 CGCGCCTCGC
 AGTGCGCAGGGTGGGTGCCCCGCGCCTGCAGCGTCCGCCGGGGCGGCGCGGGAGGTGGCCGACAG
 GCTCCGGGCC
 TCGCAGCCTCAGCCCCCGGCCAGCGCGCTTTCCGACGGCGGCGCGCCGAGCCACCCGCC
 CGCCCAAGGTCTCTCGCGGGCGGGAGAACGGAACCTCCCACTTCTGAGTTCTAAAGTTCCTGTTG
 CTTTCAACAA
 TGGATGAGCAATCACAAGGAATGCAAGGGCCACCTGTTCTCAGTTCCAACACAGAAGGCCTTACGA
 CCGGATATGG
 GCTATAATACATTAGCCAACTTTTGAATAGAAAAGAAAATTGGTCCGCGACAATTTAGTGAAG
 TTTATAGAGCAGCCTGTCTCTGGATGGAGTACCAGTAGCTTTAAAAAAGTGCAGATATTTGATTTA
 ATGGATGCCA
 AAGCAGTGTGATTGCATCAAAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAA
 TATTATGCAT
 CATTATTGAAGATAATGAACTAAACATAGTTTTTGGAACTAGCAGATGCTGGCGACCTATCCA
 GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAGTATTTTGT
 CAGCTTTGCA
 GTGCATTGGAACACATGCATTCTCGAAGAGTCATGCATAGAGATATAAAACCAGCTAATGTGTTTATT
 ACAGCCACTG
 GGGTGGTAAACTTTGGAGATCTTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCAC
 ATTCTTTAGTTGGTACGCCTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACCTCAA
 TCTGACATCT
 GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACAAAATGAAT
 TTATACTCAC
 TGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCTTTCAGATCACTATTGAGAAGAAC
 TCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAGAGAAGCGACCAGACGTCACCTATGTTTAT
 GACGTAGCAA
 AGAGGATGCATGCATGCACTGCAAGCAGCTAAACATGCAAGATCATGAAGAGTGTAACCAAAGTAATT
 GAAAGTATTT
 TGTGCAAAGTCGTACCTSCCATTATGTCTGGGTGTTAAGATTAATATTTTCAGAGCTAGTGT
 GCTCTGAATCCTTAACCAGTTTTTCATATAAGCTTCATTTTGTACCAGTCACCTAAATCACCTCCTTGC
 AACCCCCAAA
 TGACTTTGGAATAACTGAATTGCATGTTAGGAGAGAAAATGAAACATGATGGTTTTGAATGGCTAAAG
 GTTTATAGAA
 TTTCTTACAGTTTTCTGCTGATAAATTGTGTTTATAGATAGACTGTCAGTGCCAAATATTGAAGG
 TGCAGCTTGGCACCACATCAGAATAGACTCATACCTGAGAAAAAGTATCTGAACATGTGACTTGTCTTCT
 TTTTATAGTAA
 TTTATGGACATTGAGATGAACACAATTGTGAACTTTTGTGAAGATTTTATTTTTTAAACGTTTGAAGTA
 CTAGTTTTAG
 TTCTTAGCAGAGTAGTTTTCAAATATGATTCTTATGATAAATGTAGACACAACTATTTGAGA
 AACATTTAGAACTCTTAGCTTATACATTCAAATGTAACCTATTAAATGTGAAGATTTGGGGACAAAAT
 GTGAGTCAGA
 CACTGAAGAGTTTTTTGTGTTTTGTTTAAATATTTTTTGATATTCTCTTGCATTGAAATGGTATAAATGA
 ATCCATTAA
 AAAGTGGTTAAGGATTTGTTTATGCTGGTGTGATAATAATTTTTTAAAGTTGCACATTGCCCAAG
 GCTTTTTTTGTGTGTTTTATTGTTGTTTGTACATTTGAAAAATATTCTTTGAATAACCTTGCAGTAC
 TATATTTCAA

FIGURE 1

TTTCTTTATAAATTTAAGTGCATTTTAACTCATAATTGTACACTATAATATAAGCCTAAGTTTTTATT
 CATAAGTTTT
 ATTGAAGTTCTGATCGGTCCCCCTTCAGAAATTTTTTATATTATTCTTCAAGTTACTTTCTTA
 TTTATATTGTATGTGCATTTTATCCATTAATGTTTCATACTTTCTGAGAGTATAATACCCTTTTAAAA
 GATATTTGGT
 ATACCAATACTTTTCTGGATTGAAAACTTTTTTTAAACTTTTTTAAAATTTGGGCCACTCTGTATGCA
 TATGTTTGGT
 CTTGTTAAAGAGGAAGAAAGGATGTGTGTTATACTGTACCTGTGAATGTTGATACAGTTACAA
 TTTATTTGACAAGGTTGTAATTCTAGAATATGCTTAATAAAATGAAAACCTGGCCATGACTACAGCCAG
 AACTGTTATG
 AGATTAACATTTCTATTGAGAAGCTTTTGAGTAAAGTACTGTATTTGTTTCATGAAGATGACTGAGATG
 GTAACACTTC
 GTGTAGCTTAAGGAAATGGGCAGAAATTCGTAAATGCTGTTGTGCAGATGTGTTTTCCCTGAA
 TGCTTTTCGTATTAGTGGCGACCAGTTTCTCACAGAAATTGTGAAGCCTGAAGGCCAAGAGGAAGTCACT
 GTTAAAGGAC
 TCTGTGCCATCTTACAACCTTGGATGAATTATCCTGCCAACGTGAAAACCTCATGTTCAAAGAACACT
 TCCCTTTAGC
 CGATGTAACCTGCTGGTTTTGTTTTTCATATGTGTTTTTCTTACACTCATTTGAATGCTTTCAA
 GCATTTGTAACTTAAAAAAANWAWAAAGGGCAAAAAGTCTGAACCCTTGTTTTCTGAAATCTAATC
 AGTTATGTAT
 GGTTTCTGAAGGGTAATTTTATTTTGAATAGGTAAAGCGAAACCTGTTTTGTCWGTGTTTTCTGAG
 GGCTAGATGC
 ATTTTTTTTCTCACACTCTTAATGACTTTTAAACATTTATACTGAGCATCCATAGATATATTCC
 TAGAAGTATGAGAAGAATTATTCTTATTGACCATTAATGTGTCATGTTCATTTTAATGTAATATAATTGA
 GATGAAATGT
 TCTCTGGTTGGAACAGATACTCTCTTTTTTTTTCTTGCAATCTTTAAGAATACATAGATCTAAAATTC
 ATTAGCTTGA
 CCCCTCAAAGTAACTTTTAAAGTAAAGATTAAAGCTTTTCTTCTCAGTGAATATATCTGCTAGA
 AGGAAATAGCTGGGAAGAATTTAATGATCAGGGAAATTCATTATTTCTATATGTGGAACTTTTTTGCT
 TCGAATATTG
 TATCTTTTTTAAATCTAAATGTTTCATATTTTTCTGAAGAAACCACTGTGTAAAAATCAAATTTTAATT
 TTGAATGGAA
 TAATTTCAAAGAACTATGAAGATGATTTGAAGCTCTAATTTATATAGTCACCTATAAAATGTT
 CTTTATATGTGTTTCATAAGTAAATTTTATATTGATTAAGTTAACTTTTGAATTGATTTGAGGAGCAG
 TAAAATGAAA
 GCTATATCTATTNCTAAACCYTATTTAGACATTGGKACCAGTTACCCAGGTGAAAATAKGGAGTAACT
 TTGTTTTGTA
 TGGTAAGGTTTAGGAATGGNGGATGAAGGGTATCTCTATATAAATAAAGTGCTCAACAATGTG
 CAATGATTGTAAATTTAGTAAGATATTACAGCCATTTTCATGAATGCTTTACCATTCAACATAGTATCT
 ATTACAAAAC
 ACCTTTCTTGATCCATATACTTCAGGTGTTGCTGTTAACATTTACTATGATATTTATTTTAACCAAA
 ATGTTACTCA
 CATTAATGTTTATTCTTTTAAATGAATGTATTATGTTTTTAACCCACAAATGCATACTTACC
 CTGTGCCTCATATTTCAATAGTACTGTAATATGGACATCTTTGTGAAATACTTTTATTTTGTATGC
 TTTAAATATA
 CATACAAAAGATTTCTGTTATTAGCTTTGAAAATTGTATAATATCCTAATATAAACAAAAATATAAA
 AATAAAAATG
 AATACAGTAAAAAAAAAAAAAAAAAAAAAAAAAAGG .

FIGURE 1 (cont'd)

MDEQSQGMQGPVPQFQPKALRPDMGYNTLANFRIEKKIGRGQFSEVYRAACLLDGVFPVALKKVQIF
DLMDAKARAD
CIKEIDLLKQLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYFVQLC
SALEHMHSSRR
VMHRDIKPANVFITATGVVKGDLGLGRFFSSKTTAAHSLVGTPYYMSPERIHENGYNFKSDI
WSLGCLLYEMAALQSPFYGDKMNLVSLCKKIEQCDYPPLPSDHYSEELRQLVNMCIINPDPEKRPDVTY
VYDVAKRMHA
CTASS

FIGURE 1 (cont'd)

GTCGACCCACGCGTCCGGTGAAGTATAATACTTTGTCAATTATGAGATGTCGTCTCTCGG
 TGCCTCCTTTGTGCAAATTAATTTGATGACTTGCAAGTTTTTTGAAAACCTGCGGTGGAGG
 AAGTTTTGGGAGTGTATTATCGAGCCAAATGGATATCACAGGACAAGGAGGTGGCTGTAAA
 GAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTCAGTCACAGAAACAT
 CATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATTGTACAGAATATGC
 TTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAGGAGATGGATATGGA
 TCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGC
 TCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGG
 AGTACTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAA TCATACAACACACATGTC
 CTTGGTTGGAACTTCCCATGGATGGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTCAGA
 AACTTGTGACACATATTCTTATGGTGTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCC
 CTTTAAAGGTTTGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAAAAAACGAGAGATT
 AACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTGTTACATCAGTGTGGGAAGC
 TGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCATCCTGGAGTCCATGTCAAA
 TGACACGAGCCTTCCTGACAAGTGTAACCTATTCCCTACACAACAAGGCGGAGTGGAGGTG
 CGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGATCTCAGCTTTAAGGA
 GCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAAAAGCTGACAGAGCA
 GTCCAACACCCCGCTTCTCTTGCTCTTGCTGCAAGAATGTCTGAGGAGTCTTACTTTGA
 ATCTAAAACAGAGGAGTCAAACAGTGCAGAGATGTATGTGATCAGATCACAGCAACAAGTAA
 CCGGGAGGGCCATGGCATGAACCCAAGTCTGCAGGCCATGATGCTGATGGGCTTTGGGGA
 TATCTTCTCAATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAACATGCA
 AGCCAAGCAGAATTCTTCCAAAACCACATCTAAGAGAAGGGGGAAGAAAGTCAACATGGC
 TCTGGGGTTTCAAGTATTTTGAAGTGTGACGATGATGATGATGATGACGGTGA
 GGAGGAGGATAATGACATGGATAATAGTGAATGAAAGCAGAAAGCAAAGTAATAAAATCA
 CAAATGTTTGGAAAACACAAAAGTAACCTGTTTATCTCAGTCTGTACAAAAACAGTAAGG
 AGGCAGAAAGCCAAGCACTGCATTTTTTAGGCCAATCACATTTACATGACCGTAATTTCTT
 ATCAATTCTACTTTTATTTTTGCTTACAGAAAAACGGGGGGAAGTAAGCCAAAGAAGT
 ATATTTATGAATCAGCAAATGTGGTGCCTGATTATAGAAATTTGTGATCCTATATACAAT
 ATAGGACTTTTAAAGTTGTGACATTCTGGCTTTTTCTTTTAAATGAATACTTTTTAGTTTG
 TATTTGACTTTATTTCTTTTATTCAAATCATTTTTTAAAACTTACATTTTGAACAAACAC
 TCTTAACTCCTAATTGTTCTTTGACACGTAGTAATTCTGTGACATACTTTTTTTTTCTTA
 TAGCAATACACTGTAATATCAGAAATGGTTGGCCTGAGCAACCTAGTAAGACCTCGTCTC
 TACTAATAATTAAAAAACTAGCTGGCATGGTAGCACACACCTGTAGTCCCAGATACTTGG
 GAGGCCAAGGCAGGAGGATTGCTTGAGACCTAGCAATCAGTCAGGGCTGCAGTGAGCCAT
 GATGGCACCCTGCACTCTAGCCTGGGCAAGAGAACAAAGATCCTGTCTCAAAAAACAAA
 AAAAAAAAAAAGGGCGGCCG

MSSLGASFVQIKFDDLQFFENC GGGSFGSVYRAKVISQDKEVAVK
 KLLKIEKEAELSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDM
 HIMTWATDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRPHNHTHMS
 LVGTFPMAPEVIQSLPVSETCDTYSYGVVLWEMLTREVFPKGLEGLQVAVLVVEKNERL
 TIPSSCPRSFAELLHQWEADAKRPSFKQIISILEMSNDTSLPDKCNSFLHNKAEWRC
 EIEATLERLKKLERDLSFKBQELKERERRLKMWEQKLTQSNTPLLLPLAARMSEESYFE
 SKTEESNSAEMSCQITATSNEGHGMNPSLQAMMLMGFGDIFSMNKAGAVMHSGMQINMQ
 AKQNSSKTTSKRRGKKVNMALGFSDFDLSEGD DDDDDGEEEDNDMDNSE

FIGURE 2

CGGTGGTGGCGGCAGCGGCGGCTGCGGGGGCACCGGGCCGCGGCGCCACCATGGCCGTGC
 GACAGGCGCTGGGCGCGGCGCTGCAGCTGGGTGAGCGCTGCTGCTGCGCTTCACGGGCA
 AGCCCGGCGGGGCTACGGCTTGGGGCGGCGGGCCCGGCGGCGGGCTGTGTCCGCGGGG
 AGCGTCCAGGCTGGGCGCGAGGACCGGGCGCGAGCCTCGCAGGGTCGGGCTCGGGCTTC
 CTAACCGTGTCCGCTTCTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTGCAGCGGC
 AGTTTCGTGGTGGGCGCTGGGGCTGCGCGGGCCCTTGGCGGCGGGCAGTCTTTCTGGCCT
 TCGGGCTAGGGCTGGGCCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGG
 CCTGTGAGGAGATCCAGGCAATTTTACCCAGAAAAGCAAGCCGGGGCTGACCCGTTGG
 ACACGAGACGCTTGCAGGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTA
 AGGGCTGCAGTGTCTGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGG
 TGACAAAGAGCACCGGGTTGCTTCCAGGGAGAGGCCAGGTACCAGTGCACCAGGAGAAG
 GGCAGGAGCGAGTCCCGGGGCCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACA
 TCTCGGCAGGTTCTCCAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAG
 CGAGCCGAGTGGCCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAG
 GTCCCAAGCAACTAGCCCCCTCACCCCAACATCATCCGGGTCTCCGCGCCTTACCTCTT
 CCGTGCCGCTGCTGCCAGGGGCCCTGGTCGACTACCTGATGTGCTGCCCTCACGCCTCC
 ACCCTGAAGGCTGGGCCATGGCCGGACGCTGTTCTCGTTATGAAGAACTATCCCTGTA
 CCCTGCGCCAGTACCTTGTGTGAACACACCCAGCCCCCGCTCGCCGCCATGATGCTGC
 TGCAGCTGCTGGAAGCGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGA
 AATCCGACAACATCCTTGTGGAGCTGGACCCAGACGGCTGCCCCCTGGCTGGTGATCGCAG
 ATTTTGGCTGCTGCCTGGCTGATGAGAGCATCGGCCCTGCAGTTGCCCTTCAGCAGCTGGT
 ACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCTCTG
 GCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCTTGGCAGTGGGAGCCATCGCCT
 ATGAAATCTTCGGGCTTGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCC
 GCAGCTACCAAGAGGCTCAGCTACCTGCACTGCCCGAGTCAGTGCCTCCAGACGTGAGAC
 AGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCG
 CAAATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGT
 TAGACAAGATGGTTGGCTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGC
 TCACAGAGAAGTGTGTGTGGAAACAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGT
 GTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTC
 CCTGCATGGAGCTGGTGAATTACTAAAAGAACTTGGCATCCTCTGTGTGCTGATGGTCTG
 TGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAA
 AAGGCCTCGGGCTTGGCAAATGGAAGAACTTGAGTGAGAGTTCACTCTGCAGTCTCTGTC
 TCACAGACATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGA
 GGGGTAGGCCTGCATCCACAGAGAGGATCCAGGCCAAGGCACTGGCTGTGAGTGGCAGAG
 TTTGGCTGTGACCTTTGCCCCCTAACACGAGGAACCTGTTTGAAGGGGGCAGCGTAGCATG
 TCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTGAGCACGTTTCACTTACGGG
 AGTGGGAAATTACATGAGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGC
 TACTGAATTATTAATCTCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTG
 GGGATTTAAACTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATAT
 TAAATGCAAATTTACAACATGCAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCC

FIGURE 3

Met Ala

Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu
5 10 15

Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro
20 25 30

Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala
35 40 45 50

Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg
55 60 65

Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln
70 75 80

Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg
85 90 95

Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys
100 105 110

Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala
115 120 125 130

Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg
135 140 145

Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile
150 155 160

Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu
165 170 175

Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg
180 185 190

Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly
195 200 205 210

Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala
215 220 225

FIGURE 3 (cont'd)

Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu Leu Val
 230 235 240

Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val Thr Tyr
 245 250 255

Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro Asn Ile
 260 265 270

Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu Pro Gly
 275 280 285 290

Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His Pro Glu
 295 300 305

Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn Tyr Pro
 310 315 320

Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro Arg Leu
 325 330 335

Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His Leu Val
 340 345 350

Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile Leu Val
 355 360 365 370

Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp Phe Gly
 375 380 385

Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe Ser Ser
 390 395 400

Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro Glu Val
 405 410 415

Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala
 420 425 430

FIGURE 3 (cont'd)

Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val

435

440

445

450

Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
455 460 465

Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
470 475 480

Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
485 490 495

Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
500 505 510

His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
515 520 525 530

Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
535 540 545

Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
550 555 560

Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
565 570 575

Ala Ala Leu

FIGURE 3 (cont'd)

GTCGACCCACGCGGTCCGCCACGCGTTCCGGAGACATGTCTCTGTGTTTC
 TCTCCCTCCGCTTTTGAAGTCCGTTGAAGACACAATTTCTCTCTGTGCGGT
 GCTTAGGAGGAGCTCCATGAACATGTATTGAATTGGACTTAGCTGAACAG
 GCTGCTGGTTGGCTGCCAGAGGGGGCAGGCTGTGTTGCTGGGAGCCTTC
 CAGCTCCCTGCAGCAGTCATGGGGCAGGGTTCCCCGAGTCCGTAATCCCC
 ATTTCCACCTACTTTCCCTTAGTTATTTGATTCCCTGTCTGTCTGTAATCCC
 TTAAGTGGAGCATCCCCTTTCCTGGGAGACACGAAGCAGGAAACACTGGC
 AAATATCACAGCAGTGAGTTACGACTTTGATGAGGAATTCTTCAGCCAGA
 CGAGCGAGCTGGCCAAGGACTTTATTCGGAAGCTTCTGGTTAAAGAGACC
 CGGAAACGGCTCACAATCCAAGAGGCTCTCAGACACCCCTGGATCACGCC
 GGTGGACAACCAGCAAGCCATGGTGGCAGGGAGTCTGTGGTCAATCTGG
 AGAAGTTTCAAGGAAGCAGTATGTCCGCAGGCGGTGGAAGCTTTCTTCAGC
 ATCGTGTCCCTGTGCAACCACTCACCCGCTCGCTGATGAAGAAGGTGCA
 CCTGAGGCCGGATGAGGACCTGAGGAAGTGTGAGAGTGACACTGAGGAG
 GACATCGCCAGGAGGAAAGCCCTCCACCCACGGAGGAGGAGCAGCACCT
 CCTAACTGGCCTGACCTGCAGTGGCCGCCAGGGAGGTCTGGGCCCAGCGG
 GGCTCCCTTCTGTGCAGACTTTTGGACCCAGCTCAGCACCAGCACCCGGGC
 GTCCTGAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAAGAGCTT
 GCAGGCAAGCCAGGAGACCCTGGGAGCTGTGGCTGTCTTCTGTGGAGGAG
 GCTCCAGCATTCCCAAAGCTCTTAATTCTCCATAAAATGGGCTTTCTCTGT
 TCTGCCATCCTCAGAGTCTGGGGTGGGAGTGTGGACTTAGGAAAACAATA
 TAAAGGACATCCTCATCATCACGGGGTGAAGGTGAGACTAAGGCAGCCTT
 CTTACAGGCTGAGGGGGTTTCAAGAACAGCCTGGCCAAAAATTACACCAG
 AGAGACAGAGTCTTCCCCATTGGGAACAGGGTGATTGAGGAAAGTGAACC
 TTGGGTGTGAGGGACCAATCCTGTGACCTCCCAGAACCATGGAAGCCAGG
 ACGTCAGGCTGACCAACACCTCAGACCTTCTGAAGCAGCCCATTGCTGGC
 CCGCCATGTTGTAATTTTGTCTATTTTATTAACTTCTGGTTTACCTGATG
 CTTGGCTTCTTTTAGGGCTACCCCCATCTCATTTCCTTTAGCCCGTGTGCCT
 GTAAGTCTGAGGGGGGGCACCCAGTGGGGTGCTGAGTGGGCAGAATCTCA
 GAAGGTCTCTGAACCGTCCGCGCAGGCCTGCAGTGGGCCTGCCTCTC
 CTTGCTTCCCTAACAGGAAGGTGTCCAGTTCAAGAGAACCCACCCAGAGA
 CTGGGAGTGGTGGCTCACGCCTATAATCCCTGCGCTTTGGCAGTCCGAGG
 CAGGGGAATTGCTTGAAGTCAAGGAGTGGAGACCAGCCTGGGCAACATGG
 CAAAACGCAGTCTGTACAAAAAATACAAAAAATTAGCCAGGTGTAGGGGT
 AGGCACCTGGCATCCAGCTACTCCAGGGGCTGAGGTGACAGCATTGCTT
 AAGCCCAGAAGGTGAGGCTGCAGTGAAGTGAATCACGCCACTGCACTC
 CAGTCTGGGTGACAGAGAGAGACCATATCCAAAAAAGGG
 CCGCCGC

LFDSLVSLSLSPFLGDTKQETLANITAVSYDFDEEFFSQTSELAKDFIRKL
 LVKETRKRLTIQEALRHPWITPVDNQAMVRRESVNVLENFRKQYVRRRWK
 LSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKALHPRRSSTS

FIGURE 4

T A L A K E L R E L R I E E T N R P M 19
 G ACG GCA TTA GCC AAA GAA CTA AGA GAA CTC CGG ATT GAA GAA ACA AAC CGC CCA ATG 57
 K K V T D Y S S S S B E S E S S E E E E 39
 AAG AAG GTG ACT GAT TAC TCC TCC TCC AGT GAG GAG TCA GAA AGT AGC GAG GAA GAG GAG 117
 E D G E S E T H D G T V A V S D I P R L 59
 GAA GAT GGA GAG AGC GAG ACC CAT GAT GGG ACA GTG GCT GTC AGC GAC ATA CCC AGA CTG 177
 I P T G A P G S N E Q Y N V G M V G T H 79
 ATA CCA ACA GGA GCT CCA GGC AGC AAC GAG CAG TAC AAT GTG GGA ATG GTG GGG AGC CAT 237
 G L E T S H A D S F S G S I S R E G T L 99
 GGG CTG GAG ACC TCT CAT GCG GAC AGT TTC AGC GGC AGT ATT TCA AGA GAA GGA ACC TTG 297
 M I R E T S G E K K R S G H S D S N G F 119
 ATG ATT AGA GAG ACG TCT GGA GAG AAG AAG CGA TCT GGC CAC AGT GAC AGC AAT GGC TTT 357
 A G H I N L P D L V Q Q S H S P A G T P 139
 GCT GGC CAC ATC AAC CTC OCT GAC CTG GTG CAG CAG AGC CAT TCT CCA GCT GGA ACC CCG 417
 T E G L G R V S T H S Q E M D S G T E Y 159
 ACT GAG GGA CTG GGG CGC GTC TCA ACC CAT TCC CAG GAG ATG GAC TCT GGG ACT GAA TAT 477
 G A G S S T R A S F T P F V D P R V Y Q 179
 GGC ATG GGG AGC AGC ACC AAA GGC TCC TTC ACC CCC TTT GTG GAC CCC AGA GTA TAC CAG 537
 T S P T D E D E D E E S S A A A L F T 199
 ACG TCT CCC ACT GAT GAA GAT GAA GAG GAT GAG GAA TCA TCA GGC GCA GCT CTG TTT ACT 597
 S E L L R Q E Q A K L N E A R K I S V V 219
 AGC GAA CTT CTT AGG CAA GAA CAG GCC AAA CTC AAT GAA GCA AGA AAG ATT TCG GTG GTA 657
 N V N P T N I R P H S D T P E I R K Y K 239
 AAT GTA AAC CCA ACC AAC ATT CGG OCT CAT AGC GAC ACA CCA GAA ATC AGA AAA TAC AAG 717
 K R F N S E I L C A A L W G V N L L V G 259
 AAA CGA TTC AAC TCA GAA ATA CTT TGT GCA GCT CTG TGG GGT GTA AAC CTT CTG GTG GGG 777
 T E N G L M L L D R S G Q G K V Y N L I 279
 ACT GAA AAT GGC CTG ATG CTT TTG GAC CGA AGT GGG CAA GGC AAA GTC TAT AAT CTG ATC 837
 N R R R F Q Q M D V L E G L N V L V T I 299
 AAC CGG ACG CGA TTT CAG CAG ATG GAT GTG CTA GAG GGA CTG AAT GTC CTT GTG ACA ATT 897
 S G K K N K L R V Y Y L S W L R N R I L 319
 TCA GGA AAG AAG AAT AAG CTA CGA GTT TAC TAT CTT TCA TGG TTA AGA AAC AGA ATA CTA 957
 H N D P E V E K K Q G W I T V G D L E G 339
 CAT AAT GAC CCA GAA GTA GAA AAG AAA CAA GGC TGG ATC ACT GTT GGG GAC TTG GAA GGC 1017
 C I H Y K V V K Y E R I K F L V I A L K 359
 TGT ATA CAT TAT AAA GTT GTT AAA TAT GAA AGG ATC AAA TTT TTG GTG ATT GCC TTA AAG 1077
 N A V E I Y A W A P K P Y H K F M A F K 379
 AAT GCT GTG GAA ATA TAT GCT TGG GCT OCT AAA CCG TAT CAT AAA TTC ATG GCA TTT AAG 1137
 S F A D L Q H K P L L V D L T V E E G Q 399
 TCT TTT GCA GAT CTC CAG CAC AAG CCT CTG CTA GTT GAT CTC ACG GTA GAA GAA GGT CAA 1197
 R L K V I F G S H T G F H V I D V D S G 419

FIGURE 5

AGA	TTA	AAG	GTT	ATT	TTT	GGT	TCA	CAC	ACT	GGT	TTC	CAT	GTA	ATT	GAT	GTT	GAT	TCA	GGA	1257
N	S	Y	D	I	Y	I	P	S	H	I	Q	G	N	I	T	P	H	A	I	439
AAC	TCT	TAT	GAT	ATC	TAC	ATA	CCA	TCT	CAT	ATT	CAG	GGC	AAT	ATC	ACT	CCT	CAT	GCT	ATT	1317
V	I	L	P	K																
GTC	ATC	TTC	CCT	AAA																444
																				1332

FIGURE 5 (cont'd)